

1    LEGENDS FOR SUPPLEMENTARY FILES

2    **Supplementary File 1:** *Excel file with the results of SpeciesFinder, rMLST,*  
3    *TaxonomyFinder, and KmerFinder on the NCBI<sub>drafts</sub> set.*

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5    **Supplementary File 2:** *Predictions for the most common species of the NCBI<sub>drafts</sub>*  
6    *set SpeciesFinder (page 1), rMLST (page 2), KmerFinder (page 3), TaxonomyFinder*  
7    *(page 4), and whole-genome BLAST-based method (page 5). For each method, the*  
8    *results for a given species is only shown if the method made a prediction for five or*  
9    *more isolates annotated as this species, or two or more isolates are predicted as*  
10    *this species. Predictions for the most common species of the SRA<sub>drafts</sub> set by*  
11    *SpeciesFinder (page 6), rMLST (page 7), KmerFinder (page 8), TaxonomyFinder*  
12    *(page 9), and whole-genome BLAST-based method (page 10). For each method, the*  
13    *results for a given species is only shown if the method made a prediction for ten or*  
14    *more isolates annotated as this species, or two or more isolates are predicted as*  
15    *this species.*

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17    LEGENDS FOR SUPPLEMENTARY FIGURES

18    **Supplementary Figure 1:** *Distribution of N50 values for the draft genomes of the*  
19    *SRA<sub>drafts</sub> set.*

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21    **Supplementary Figure 2:** *Predictions for the most common species in the SRA<sub>reads</sub>*  
22    *dataset. Only predictions for species that occur 10 or more times in the dataset are*  
23    *shown. Only species that are predicted two or more times are shown. A: Predictions*  
24    *by the SpeciesFinder method. B: Predictions by the KmerFinder method. C:*  
25    *Predictions by the Reads2Type method.*

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2 LEGENDS FOR SUPPLEMENTARY TABLES

3 ***Supplementary Table 1: Overview of the training data.***

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5 ***Supplementary Table 2: Overview of the NCBI<sub>drafts</sub> evaluation set.***

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7 ***Supplementary Table 3: Overview of the SRA<sub>drafts</sub> and SRA<sub>reads</sub> evaluation sets.***

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